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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=9; day=1; hr=14; min=39; sec=46; ms=709; ]

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\*\*\*\*\*

Reviewer Comments:

<160> US 60/550,014

<161> 2004-03-03

<170> 8

<180> PatentIn version 3.4

Please change the Numeric identifier <160> and <161> to <150> and <151>, since <150> and <151> represents Prior Application Number and Date.

Numeric Identifier <170> to <160>, which represents the Total Number of Sequences in the sequence listing.

Numeric Identifier <180> to <170> which represents Software type. It should appear as below:

<150> US 60/550,014

<151> 2004-03-03

<160> 8

<170> PatentIn version 3.4

Please make all necessary changes.

\*\*\*\*\*

Application No: 10591486 Version No: 1.0

Input Set:

Output Set:

Started: 2010-08-26 11:28:55.496  
 Finished: 2010-08-26 11:29:01.799  
 Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 303 ms  
 Total Warnings: 4  
 Total Errors: 19  
 No. of SeqIDs Defined: 0  
 Actual SeqID Count: 8

Error code	Error Description
E 202	Invalid input format; Value must be an integer in <160>
E 104	Command to process tag does not exist: Tag: <161> in Header
E 248	Order Sequence Error <160> -> <161>; Expected Mandatory Tag: <210> in Header
E 104	Command to process tag does not exist: Tag: <180> in Header
E 248	Order Sequence Error <170> -> <180>; Expected Mandatory Tag: <210> in Header
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)

**Input Set:**

**Output Set:**

**Started:** 2010-08-26 11:28:55.496  
**Finished:** 2010-08-26 11:29:01.799  
**Elapsed:** 0 hr(s) 0 min(s) 6 sec(s) 303 ms  
**Total Warnings:** 4  
**Total Errors:** 19  
**No. of SeqIDs Defined:** 0  
**Actual SeqID Count:** 8

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 252	Calc# of Seq. differs from actual; 0 seqIds defined; count=8
E 250	Structural Validation Error; Sequence listing may not be indexable

# SEQUENCE LISTING

<110> Waugh, Jacob  
Dake, Michael

<120> Compositions and Methods for Topical Diagnostic and Therapeutic  
Transport

<130> 13720-105068US2

<140> US 10/591,486

<141> 2007-06-18

<150> US 11/073,307

<151> 2005-03-03

<160> US 60/550,014

<161> 2004-03-03

<170> 8

<180> PatentIn version 3.4

<210> 1

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MOD\_RES

<222> (1)..(20)

<223> This region may encompass 0 to 20 Gly residues

<220>

<221> MOD\_RES

<222> (1)..(45)

<223> See specification as filed for detailed description of  
substitutions and preferred embodiments

<220>

<221> MOD\_RES

<222> (21)..(45)

<223> This region may encompass an odd number of Arg residues from 5 to  
25

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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
1 5 10 15

Gly Gly Gly Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg  
20 25 30

Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg  
35 40 45

<210> 2  
<211> 51  
<212> PRT  
<213> Human immunodeficiency virus

<220>  
<221> misc\_feature  
<222> (1)..(51)  
<223> See specification as filed for detailed description of  
substitutions and preferred embodiments

<220>  
<221> MOD\_RES  
<222> (32)..(51)  
<223> This region may encompass 0 to 20 residues

<220>  
<221> MOD\_RES  
<222> (32)..(51)  
<223> This region may encompass 0 to 20 residues

<400> 2

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
1 5 10 15

Gly Gly Gly Gly Arg Gly Arg Asp Asp Arg Arg Gln Arg Arg Arg Gly  
20 25 30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
35 40 45

Gly Gly Gly  
50

<210> 3  
<211> 51  
<212> PRT  
<213> Human immunodeficiency virus

<220>  
<221> MOD\_RES  
<222> (1)..(20)  
<223> This region may encompass 0 to 20 Gly residues



Gly Gly Gly Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Gly  
20 25 30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
35 40 45

Gly

<210> 5  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 5

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1 5 10

<210> 6  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<220>  
<221> MOD\_RES  
<222> (1)..(5)  
<223> This region may encompass 3 to 5 Gly residues

<220>  
<221> MOD\_RES  
<222> (1)..(22)  
<223> See specification as filed for detailed description of  
substitutions and preferred embodiments

<220>  
<221> MOD\_RES  
<222> (5)..(22)  
<223> This region may encompass an odd number of Arg residues from 7  
through 17

<400> 6

Gly Gly Gly Gly Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg  
1 5 10 15

Arg Arg Arg Arg Arg Arg  
20

<210> 7  
<211> 12  
<212> PRT  
<213> Human immunodeficiency virus

<400> 7

Gly Gly Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 8  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

<400> 8

Arg Arg Arg Arg Arg Arg Arg Arg Arg  
1 5